



```

61  l u a s n l y s v a l a s n g l u a s p g l y p h e l e u v a l m e t l e u s e r l y s g l y 77
    |||
102 a s a t t a a a c t a t g a t g g t t c t a g t t c a t g c t t a g t a a g g t 151
    |||
78  l y s t h r s e r g l y s e r t h r c l y t h r s e r s e r g l n h i s e r s a n t h r p 94
    |||
152 a a a a c t c t g g t t c a c t g a a c t t c a t c t c c a c a c t c a a a c t c c 201
    |||
94  o a l a t h r a t g l n a l a p r o p r o l e u g l u a l a p r o g l n g l n a l a p r o g l n p 111
    |||
202 t g c a c a a g c a g c a g c a c t c t c t a g a g c c c a c a a c a a g c t c c a n c 251
    |||
111 r o p r o v a l a p r o l i e t h r t h r s e r g l n p r o g l u g l y l e u p r o a l a g l n 127
    |||
252 c c c c g t g c a c c a a t t a c a c t t c t a c c t g a m a g a c t t c c t g c a c a g 301
    |||
128 a l a p r o a n t h r h i s a s p a n a l a s e r a s n l e u s e r g l y a r g a s 144
    |||
302 g c a c c t a a c a c a t g a c a t g c g c a t c a a n t c t t c t g t g a a g a a 351
    |||
144 n v a l a s p t h r l i e l e a s n g l n l e u m e t g l u m e t g l y g l y s e r t r p a 161
    |||
352 t g t t g a c a c a a t a t t a a c c a g t a t g a g a t g g t g g g a a g t t g g g 401
    |||
161 s p l y s 162
    |||
402 a c a a a 406

seq_name: gb_est2:BE510591

seq_documentation block:
LOCUS BE510591 365 bp mRNA linear EST 07-AUG-2000
DEFINITION 94605404.x1 946 - tassal primordium prepared by schmidt lab Zea
ACCESION BE510591
VERSION BE510591.1 GI:9731839
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoidae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 365)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
University
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 946054 row: A column: 04.
FEATURES
Source location/Qualifiers
1..365 /organism="Zea mays"
/cultivar="OH43"
/db_xref="taxon:4577"
/clone_lib="946 - tassal primordium prepared by Schmidt
lab"
/issue_type="tassels"
/dev_stage="just after the transition from vegetative to
inflorescence development"
/lab_host="X10LR"
/note="Organ: tassels; Vector: HybriZAP; Site_1: EcorI;
Site_2: XhoI; George Chuck dissected immature tassels
between 1mm and 3mm. Sharon Stanfield prepared the cDNA
library in HybriZAP. Sample insert size range was 350 bp
to 3 kb with a 1 kb average."
BASE COUNT 94 a 99 c 77 g 95 t
ORIGIN

```

```

alignment_scores:
    Quality: 121.00      Length: 121
    Ratio: 1.000        Gaps: 0
    Percent Similarity: 100.000    Percent Identity: 100.000

alignment_block:
US-09-805-550-4 x BE510591/rev ..

Align seg 1/1 to reverse of: BE510591 from: 1 to: 365

223 ProleuaspLeuPheProGlnGlyAlaSerAsnAlaGlyGlyAlaGcl 239
    |||
363 CCACGTAGATCTTTCCCGAGGGGGCTTCCAAATGTGAGAGTGCTGCG 314
    |||
239 YGlyGlyProLeuAspPheLeuArgAsnAsnProGlnPheGlnAlaVala 256
    |||
313 TGGTGGACCACTTGATTTCTTAGAAACAATCCACAGTTTCAAGCAGTTC 264
    |||
256 rglumetValHisThrAsnProGlnIleLeuGlnProMetLeuValGlu 272
    |||
263 GGGAAATGGTCCATACAAATCCACAATTTTGAGCCTATGCTGTTGAG 214
    |||
273 LeuSerLySGlnAsnProGlnIleLeuArgLeuIleGluGluAsnHisAs 289
    |||
213 TTGAGCAGACGAGAAATCCTCAAAATTTAAGGTGATTGAGAGAAATCATGA 164
    |||
289 pgluPheLeuGlnLeuLeuAsnGluProPheGluGlyGlyGlyAsp 306
    |||
163 TGAATTCTTCACTTAATATGAGCCCTTTGAAGCGGGAGAGGGGAT 114
    |||
306 heLeuAspGlnProGluGluAspGluMetProHisAlaIleSerValThr 322
    |||
113 TCTTAGCCCACTGAGAGAGATGAATGCTTCAGCCATTAAGTTTAC 64
    |||
323 ProGluGluGlnGluAlaIleGlyArgLeuGluSerMetGlyPheAsp 339
    |||
63 CCAGAGAGAGCAGAGAGGCAATGGAGCGCTTGCATGCGGTTCCAGACAG 14
    |||
339 gAlaArgValIle 343
    |||
13 AGCACCGCTTATC 1

seq_name: gb_est1:A1901927

seq_documentation block:
LOCUS A1901927 479 bp mRNA linear EST 27-JUL-1999
DEFINITION 618012805.x1 618 - Inbred Tassel cDNA Library Zea mays cDNA, mRNA
sequence.
ACCESION A1901927
VERSION A1901927.1 GI:5608260
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoidae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 479)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
University
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 618012 row: E column: 05.
FEATURES
Source location/Qualifiers
1..479

```

/organism="Zea mays"  
 /cultivar="Ohio43"  
 /db\_xref="taxon:4577"  
 /clone\_lib="618 - Inbred Tassel cDNA library"  
 /tissue\_type="tassel"  
 /dev\_stage="tassel length from 0.1 to 2.5 cm"  
 /lab\_host="XLOLR"  
 /note="Organ: tassel; Vector: pAD-GAL4-2.1 (Hybridap);  
 Inbred tassel library from Schmidt lab"

BASE COUNT 139 a 126 c 97 g 117 t  
 ORIGIN

alignment\_scores:  
 Quality: 101.00 Length: 101  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
 US-09-805-550-4 x AI901927/rev ..

Align seg 1/1 to reverse of: AI901927 from: 1 to: 479

268 PrometleuValGluLeuSerLysGlnAspProGlnIleLeuArgLeuI 284  
 ||||||||||||||||||||||||||||||||||||||||||||||||  
 478 CCTATGCTCGTTGAGTTCAGCAAGCAATCTCAATCTCAAGTTGAT 429  
 ||||||||||||||||||||||||||||||||||||||||||||||||  
 284 eglGluAsnHisAspGluPheLeuGlnLeuLeuAsnGluProPheGlu 301  
 ||||||||||||||||||||||||||||||||||||||||||||||||  
 428 TGAGGAGAAATCATGATGATGATTCTTCAGTTACTAATGAGCCCTTTAG 379  
 ||||||||||||||||||||||||||||||||||||||||||||||||  
 301 LylGluGluGlyAspPheLeuAspGlnProGluGluAspGluMetProHis 317  
 ||||||||||||||||||||||||||||||||||||||||||||||||  
 378 GCGGAGAGGCGGATTTCTTAGACCACTGAGAGATGAATGCTCTCAC 329  
 ||||||||||||||||||||||||||||||||||||||||||||||||  
 318 AlAlIleSerValThrProGluGluGlnGluAlaIleGlyArgLeuGlu 334  
 ||||||||||||||||||||||||||||||||||||||||||||||||  
 328 GCATTATGATTACACCAAGAGAGAGAGGCGCTTGAGCGCTTGAGTC 279  
 ||||||||||||||||||||||||||||||||||||||||||||||||  
 334 rmetGlyPheAspParGlyAlaArgValIleGluAlaPheLeuAlaCysAsp 351  
 ||||||||||||||||||||||||||||||||||||||||||||||||  
 278 CATGGGGTTGACAGACAGCAGCGTTATCGAAGCTTTTAGCCGCGATA 229  
 ||||||||||||||||||||||||||||||||||||||||||||||||  
 351 rGAsnGluGluLeuAlaAlaAsnTyrLeuLeuGluHisAlaGlyGluGlu 367  
 ||||||||||||||||||||||||||||||||||||||||||||||||  
 228 GGAACGAGGAGTAGCAGCAAACTATCTCTTGAGCATGCTGCGAGGAA 179  
 ||||||||||||||||||||||||||||||||||||||||||||||||  
 368 Asp 368  
 ||||  
 178 GAT 176

seq\_name: gb\_est2:BF655703

seq\_documentation\_block:

LOCUS BF655703 315 bp mRNA linear EST 20-DEC-2000  
 DEFINITION F01\_47\_H02\_b1\_A003 Floral-induced Meristem 1 (F01) Sorghum  
 propinquum cDNA, mRNA sequence.

ACCESSION BF655703  
 VERSION BF655703.1 GI:11920835  
 KEYWORDS EST.  
 SOURCE Sorghum propinquum.  
 ORGANISM Sorghum propinquum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
 clade; Panicoideae; Andropogoneae; Sorghum.  
 1 (bases 1 to 315)  
 Cordonnier-Pratt,M.-M., Gingle,A., Sudman,M., Marsala,C. and Pratt  
 ,L.H.  
 An EST database from Sorghum: floral-induced meristems  
 Unpublished (2000)  
 Contact: Cordonnier-Pratt MM  
 Department of Botany  
 The University of Georgia

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
 Tel: 706 542 1860  
 Fax: 706 542 1805  
 Email: mmp@prattuga.edu  
 Sequences have been trimmed to exclude polyA, vector and regions  
 below paired quality 16. The threshold for highest quality sequence  
 is 20.  
 Seq primer: JEN REV  
 High quality sequence start: 54  
 High quality sequence stop: 217  
 POLYA=No.

#### FEATURES

##### source

1. 315 Location/Qualifiers  
 /organism="Sorghum propinquum"  
 /db\_xref="taxon:132711"  
 /clone\_lib="Floral-induced Meristem 1 (F01)"  
 /note="Organ: Floral-induced meristems; Vector:  
 pBluescript II from Lambda Zap II; Site\_1: XhoI; Site\_2:  
 EcoRI; mature plants were placed in a growth chamber for  
 15 days with 16 hr darkness and 8 hr light (flowering is  
 induced by short-day conditions); 16 days after being  
 returned to the greenhouse under natural long days during  
 late April/early May, meristems were harvested The  
 library was made from poly-A RNA in the cloning vector  
 lambda Zap II. Clones to be sequenced were prepared by  
 mass excision."

BASE COUNT 82 a 96 c 91 g 46 t  
 ORIGIN

alignment\_scores:  
 Quality: 59.00 Length: 59  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
 US-09-805-550-4 x BF655703 ..

Align seg 1/1 to: BF655703 from: 1 to: 315

1 MetLysLeuThrValLysThrLeuLysGlyThrHisPheGluIleArgVa 17  
 ||||||||||||||||||||||||||||||||||||||||||||||||  
 137 ATGAAGCTGACGGTGAAAGACCTCAAGGGCAGCGCTTCGAGATCCGGGT 186  
 ||||||||||||||||||||||||||||||||||||||||||||||||  
 17 LglProAsnAspThrIleMetAlaValLysLysAsnIleGluGlu 34  
 ||||||||||||||||||||||||||||||||||||||||||||||||  
 187 GCAGCCCAACAGCACAGATATGCGCTGCAAGAAAAACATCCAAGATAC 236  
 ||||||||||||||||||||||||||||||||||||||||||||||||  
 34 lngLysAspSerTyrProTrrpGluGlnGluLeuIlePheAsnGly 50  
 ||||||||||||||||||||||||||||||||||||||||||||||||  
 237 AAGGAAAGGACAGCATTCATCGGGGCAACAACGTGATTTCAATGGG 286  
 ||||||||||||||||||||||||||||||||||||||||||||||||  
 51 LysValLeuLysAspGluSerThrLeu 59  
 ||||||||||||||||||||||||||||||||||||||||||||||||  
 287 AAGGCTTGAAAGATGAAGATACATG 313

seq\_name: gb\_est2:BE360535

seq\_documentation\_block:

LOCUS BE360535 605 bp mRNA linear EST 20-JUL-2000  
 DEFINITION D01\_64\_F06\_b1\_A002 Dark Grown 1 (D01) Sorghum bicolor cDNA, mRNA  
 sequence.

ACCESSION BE360535  
 VERSION BE360535.1 GI:9302092  
 KEYWORDS EST.  
 SOURCE Sorghum.  
 ORGANISM Sorghum bicolor  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
 clade; Panicoideae; Andropogoneae; Sorghum.  
 1 (bases 1 to 605)  
 Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and Pratt  
 ,L.H.

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

TITLE An EST database from Sorghum: dark-grown seedlings  
JOURNAL Unpublished (2000)  
COMMENT Contact: Cordonnier-Pratt MM  
Department of Botany  
The University of Georgia  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 542 1805  
Email: mmpratt@uga.edu  
Sequences have been trimmed to exclude PolyA, vector and regions below phred quality 16. The threshold for highest quality sequence is 20.  
Seq primer: JEN REV  
High quality sequence stop: 567  
POLYA-No.

FEATURES  
source location/Qualifiers  
1..605  
/organism="Sorghum bicolor"  
/db\_xref="taxon:4558"  
/clone\_id="Dark grown 1 (DG1)"  
/note="Organ: 5-day-old dark-grown seedlings; Vector: lambda zap; Site 1: XhoI; Site 2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision."

BASE COUNT 166 a 178 c 152 g 109 t  
ORIGIN

alignment\_scores:  
Quality: 59.00 Length: 59  
Ratio: 1.000 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
US-09-805-550-4 x BE360535 ..

Align seg 1/1 to: BE360535 from: 1 to: 605

1 MetTysLeuThrValLysThrLeuLysGlyThrHisPheGluIleArgVa 17  
|||||  
148 ATGAAGCTGACGCGTGAAGACCTCAAGGCGACGACCTCGAATCCGGGT 197  
|||||  
17 TGlntroAnaSpThrIleMetAlaValLysAsnIleGluGluIleG 34  
|||||  
198 GCAGCCCAACGACGACGATGATGGCTGTGAAGAAAGACATCGAAGATAC 247  
|||||  
34 TnglyLysAspSerTyrProTrpGlyGlnGlnLeuLeuIlePheAsnGly 50  
|||||  
248 AAGGAAAGACAGCTATTCATGCGGGGCAACACTGCTGATTTCATATGG 297  
|||||  
51 LysValLeuLysAspGluSerThrLeu 59  
|||||  
298 AAGGCTCTGAAAGATGAAGTACATTCG 324

seq\_name: gb\_estl:AI612200

seq\_documentation\_block:  
LOCUS AI612200 374 bp mRNA linear EST 21-APR-1999  
DEFINITION 486083C02.x1 486 - leaf primordia cDNA library from Hake lab Zea mays cDNA, mRNA sequence.  
ACCESSION AI612200  
VERSION AI612200.1 GI:4621367  
KEYWORDS EST.  
SOURCE Zea mays.  
ORGANISM Zea mays.  
Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 374)  
AUTHORS Walbot,V.  
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University  
JOURNAL Unpublished (1999)

COMMENT Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 486083 row: C column: 02.

FEATURES  
source location/Qualifiers  
1..374  
/organism="Zea mays"  
/cultivar="B73"  
/db\_xref="taxon:4577"  
/clone\_id="486 - leaf primordia cDNA library from Hake lab"  
/tissue\_type="leaf primordia"  
/dev\_stage="p7-p11 leaf"  
/lab\_host="E.coli XL1-Blue MFR"  
/note="Organ: Shoot; Vector: Lambda zap; Hake lab cDNA library."

BASE COUNT 96 a 93 c 59 g 126 t  
ORIGIN

alignment\_scores:  
Quality: 58.00 Length: 58  
Ratio: 1.000 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:  
US-09-805-550-4 x AI612200/rev ..

Align seg 1/1 to reverse of: AI612200 from: 1 to: 374

311 GUGLUASPGlUmeProHisAlaIleSerValThrProGluGluGlnG 327  
|||||  
373 GAGGAGATGAATGCTCATGCTATGCTTACGCCAGAGACGACGAGA 324  
|||||  
327 uAlaIleGlyArgLeuGluSerMetGlyPheAspArgAlaArgValIleG 344  
|||||  
323 GGCATTGGACGCGCTTGACTCATGGCGGTTCAGACAGACGCGTATATG 274  
|||||  
344 LuAlaPheLeuAlaCysAspArgAsnGluGluLeuAlaAlaAsnTyrLeu 360  
|||||  
273 AAGCATCTTACCTGCGCTAGGAGAGACGACGACCAACTATCTC 224  
|||||  
361 LeuGluHisAlaGlyGluLysP 368  
|||||  
223 CTTGACATGCTGCTGAGGAGAT 200

seq\_name: gb\_estl:AW171897

seq\_documentation\_block:  
LOCUS AW171897 603 bp mRNA linear EST 12-NOV-1999  
DEFINITION 618053E05.x1 618 - Indred Tassel cDNA library Zea mays cDNA, mRNA sequence.  
ACCESSION AW171897  
VERSION AW171897.1 GI:6403422  
KEYWORDS EST.  
SOURCE Zea mays.  
ORGANISM Zea mays.  
Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 603)  
AUTHORS Walbot,V.  
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University  
JOURNAL Unpublished (1999)  
COMMENT Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Plate: 618053 row: E column: 05.  
 Location/Qualifiers  
 1. 603

FEATURES  
 source  
 /organism="Zea mays"  
 /cultivar="Ohio43"  
 /db\_xref="taxon:4577"  
 /clone\_lib="618 - Inbred Tassel cDNA library"  
 /tissue\_type="tassel"  
 /dev\_stage="tassel length from 0.1 to 2.5 cm"  
 /lab\_host="XLOLR"  
 /note="Organ: tassel; Vector: PAD-GAL4-2.1 (Hybridap);  
 Inbred tassel library from Schmidt lab"  
 BASE COUNT 173 a 114 c 149 g 167 t  
 ORIGIN

## alignment\_scores:

Quality: 56.00 Length: 56  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

## alignment\_block:

US-09-805-550-4 x AM171897 ..

Align seg 1/1 to: AM171897 from: 1 to: 603

313 AAGGLMEFroHSAHAIIESerValThProGluGluGluGluAlaI1 329  
 ||||||||||||||||||||||||||||||||||||||||||||  
 297 GATGAAATGCTCACGCCATTAGTTCACACAGAGAGAGAGGCCAT 346  
 329 eGIYATgLeuGluSerMetGlyPheAsPArgAlaArGValI1eGluAlaP 346  
 ||||||||||||||||||||||||||||||||||||||||||||  
 347 TGAACGGCTTGATCCATGGGTTCCACAGACGCGCTTATCGAACAT 396  
 346 heLeuAlaCyAsPArgAsnGluGluLeuAlaAlaAsnTYrLeuLeuGlu 362  
 ||||||||||||||||||||||||||||||||||||||||||||  
 397 TCTTACGCTCGATAGACAGACAGAGAGTACGACAACTATCTCTTACG 446  
 363 HIsAlaGlyGluGluAsp 368  
 ||||||||||||||||||||||||||||||||||||||||||||  
 447 CATGCTGTTGAGGAAGAT 464

seq\_name: gb\_est1:AA61449

## seq\_documentation\_block:

LOCUS AA61449 220 bp mRNA linear EST 12-NOV-1997  
 DEFINITION ZEST00631 Maize leaf, StraiGene #937005 Zea mays cDNA clone  
 csuh00631 5' end similar to RAD 23, mRNA sequence.

ACCESSION AA61449  
 VERSION AA61449.1 GI:2615440

KEYWORDS EST.  
 SOURCE Zea mays.

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
 clade; Panicoidae; Andropogoneae; Zea.  
 1 (bases 1 to 220)

## REFERENCE

1 (bases 1 to 220)

Baydortler, C.  
 The Maize cDNA Program

## AUTHORS

Unpublished (1993)

## JOURNAL

Contact: Baydortler C  
 California State University

Dept Biol Sci, California State Univ, Hayward, CA 94542

Tel: 5108854747

Fax: 5108854747

Email: cbaysdor@haywire.csu Hayward.edu

## FEATURES

Seq primer: SK.

Location/Qualifiers  
 1..220  
 /organism="Zea mays"

/strain="B73"  
 /db\_xref="taxon:4577"  
 /clone="csuh00631"  
 /clone\_lib="Maize leaf, StraiGene #937005"  
 /note="Vector: Uni-ZAP; Site\_1: EcoRI; Site\_2: XhoI; mRNA  
 isolated from illuminated leaves and sheaths of 5 week old  
 plant. cDNA directionally cloned into vector."  
 BASE COUNT 48 a 60 c 56 g 53 t  
 ORIGIN

## alignment\_scores:

Quality: 41.00 Length: 41  
 Ratio: 1.000 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

## alignment\_block:

US-09-805-550-4 x AA61449 ..

Align seg 1/1 to: AA61449 from: 1 to: 220

202 AlAsnThrThrAsPArgAlaProThrGlyGluAlaGlyLeuSerGlyI1 218  
 ||||||||||||||||||||||||||||||||||||||||||||  
 94 GCAACACACTGATCGAGCTCTACTGAGGAGAGCTGCTCTGGAT 143  
 218 eProAsnThrAlaProLeuAsPLeuPheProGluGlyAlaSerAsnAlaG 235  
 ||||||||||||||||||||||||||||||||||||||||||||  
 144 TCCAACACCGCTCCACTAGATCTTTCCGCGAGGGGCTTCATGCTG 193  
 235 lYgIyGlyAlaGlyGlyPro 242  
 ||||||||||||||||||||||||||||||||||||||||||||  
 194 GAGGTGGTGGTGGTGGTGGACCA 216

seq\_name: gb\_est1:A1948181

## seq\_documentation\_block:

LOCUS A1948181 460 bp mRNA linear EST 19-AUG-1999  
 DEFINITION 603037D08.x1 603 - stressed root cDNA library from Wang/Bohnert lab  
 Zea mays cDNA, mRNA sequence.

ACCESSION A1948181  
 VERSION A1948181.1 GI:5740491

KEYWORDS EST.

SOURCE Zea mays.

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
 clade; Panicoidae; Andropogoneae; Zea.  
 1 (bases 1 to 460)

Maize ESTs from various cDNA libraries sequenced at Stanford

University

Unpublished (1999)

Contact: Walbot V

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Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 603037 row: D column: 08.

Location/Qualifiers

1..460

## FEATURES

source

/organism="Zea mays"

/cultivar="B73"

/db\_xref="taxon:4577"

/clone\_lib="603 - stressed root cDNA library from

Wang/Bohnert lab"

/tissue\_type="seedling"

/dev\_stage="salt stress"

/lab\_host="E. coli XL Gold"

/note="Organ: root; Vector: pBluescriptII SK(+); XR;  
 Seedling stressed root cDNA library from Wang/Bohnert lab"

## BASE COUNT

126 a 114 c 85 g 135 t

## ORIGIN

alignment\_scores:                    Quality:    39.00                    Length:    39  
                                       Ratio:       1.000                    Gaps:       0  
 Percent Similarity: 100.000        Percent Identity: 100.000

## alignment\_block:

US-09-805-550-4 x A1948181/rev ..

Align seg 1/1 to reverse of: A1948181 from: 1 to: 460

330 G1YAAGLEUGLUSERTCGLYPHEASPARGALAAAGVAILLEGLUALAPH 346  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 331 GGACGCGCTTGAGTTCATGGGCTTCGACAGACGCGCTTATGAAACATT 282  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 346 ELEUALCYSASPARGASNGLUGLULEUALAALASNTYRLLEUGLUNH 363  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 281 CTTACCTCGCGATTAGGACGAGAGAGCTACGACCAACTATCTCTTGAGC 232

363 ISALAGLYGLUGLUNASP 368  
 ||||||||||||||||||

231 ATGCTGTGAGGAGAGACT 215

seq\_name: gb\_gss: BH255752

seq\_documentation\_block:

LOCUS BH255752 463 bp DNA linear GSS 29-NOV-2001

DEFINITION LDH5BAM0003D09f Zea mays L. DH5alpha methyl filtration maize leaf

genomic shotgun library Zea mays genomic clone LDH5BAM0003D09f, DNA

sequence.

ACCESSION BH255752 GI:17150645

VERSION BH255752.1

KEYWORDS GSS.

SOURCE Zea mays.

ORGANISM Zea mays.

REFERENCE Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC

1 (bases 1 to 463)

Kim, S.-W., Yu, Y., Lee, M.-C., Yang, T.-J., Main, D., Henry, D., Oates, R.

and Wing, R.A.

TITLE Genomic shotgun library from maize

JOURNAL Unpublished (2001)

COMMENT Contact: Wing RA

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: rwing@clemson.edu

Seq primer: TAATACGACTCATATAGG

Class: shotgun

High quality sequence stop: 358.

Location/Qualifiers

1..463

/organism="Zea mays"

/strain="B73"

/db\_xref="taxon:4577"

/clone="LDH5BAM0003D09f"

/clone\_lib="Zea mays L. DH5alpha methyl filtration maize

leaf genomic shotgun library"

/lib\_host="DH5alpha"

/note="Vector: pCUGIBL-1; Site 1: Sau3A1; Site 2: Sau3A1;

Methyl filtration library, Nuclei DNA was digested with

Sau3A1, size fractionated and transformed to

E.coli DH5alpha."

BASE COUNT 109 a 92 c 90 g 168 t 4 others

ORIGIN

## alignment\_scores:

Quality:    37.00                    Length:    37  
                                       Ratio:       1.000                    Gaps:       0  
 Percent Similarity: 100.000        Percent Identity: 100.000

## alignment\_block:

US-09-805-550-4 x BH255752 ..

Align seg 1/1 to: BH255752 from: 1 to: 463

268 PrometleuValGluLeuSerLysGlnAsnProGlnIleLeuArgLeuI 284  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 74 CCTATCTCTGCTTGAGTTGAGACAGACGAAATCCCAATTTCTAAGTTGAT 123  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 284 egluIuaSnHIsAspGluPhelLeuGluLeuAsnGluProPheGluG 301  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 124 TGAGGAGAAATCATGATGATGTTCTTCACTTAATGAGCCCTTGAAAG 173  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 301 lylGlyGluGly 304  
 ||||||||||||||||

174 GCGAGAGAGGGG 184

seq\_name: gb\_est2: BE471046

seq\_documentation\_block:

LOCUS BE471046 409 bp mRNA linear EST 28-JUL-2000

DEFINITION WHE0283\_E11\_121S wheat drought-stressed seedling cDNA library

Trilicium aestivum CDNA clone WHE0283\_E11\_121, mRNA sequence.

ACCESSION BE471046

VERSION BE471046.1 GI:9561525

KEYWORDS EST.

SOURCE bread wheat.

ORGANISM Trilicium aestivum

Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae

1 (bases 1 to 409)

Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han

, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J.,

Seaton, C.L. and Tong, J.C.

The structure and function of the expressed portion of the wheat

genomes - Drought-stressed seedling cDNA library

Unpublished (2000)

COMMENT Contact: Olin Anderson

US Department of Agriculture, Agriculture Research Service, Pacific

West Area, Western Regional Research Center

800 Buchanan Street, Albany, CA 94710, USA

Tel: 5105595773

Fax: 5105595818

Email: oanderson@nrcp.usda.gov

Sequence have been trimmed to remove vector sequence and low

quality sequence with phred score less than 20

Seq primer: Stratagene SK primer.

Location/Qualifiers

1..409

/organism="Trilicium aestivum"

/cultivar="Chinese Spring"

/db\_xref="taxon:4565"

/clone="WHE0283\_E11\_121"

/clone\_lib="Wheat drought-stressed seedling cDNA library"

/lib\_host="E. coli SOLR"

/note="Vector: Lambda Uni-ZAP XR, excised phagemid;

Site 1: EcoRI; Site 2: XhoI; Seeds were surface-sterilized

, germinated and grown aseptically in the dark at room

temperature on filter paper with water, nystatin and

ceftioaxime in covered crystallization dishes. Five-day old

seedlings were incubated for one day at 90° RH. After

removing endosperm, seedlings were transferred to

dessicator jar containing saturated MgSO4 at room

temperature for 24 hr. The tissue, total RNA, and poly(A)

RNA were prepared, a cDNA library was made, and the cDNA

clones were in vivo excised to give pBluescript phagemids in the T3 Close Lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

BASE COUNT 119 a 94 c 125 g 71 t

ORIGIN

alignment\_scores:

Quality:	28.00	Length:	28
Ratio:	1.000	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	100.000

alignment\_block:

US-09-805-550-4 x BE471046 ..

Align seg 1/1 to: BE471046 from: 1 to: 409

20 AsnAspThrIleMetAlaValLysAsnIleGluGlnIleGlnGly 36  
|||||  
226 AATGACACCATATGCTGCTCAGAGAACATTCAGATTCAGAGAAA 275

36 SASPSerTyrProTrrpGlyGlnGlnLeuIle 47  
|||||  
276 GGATAGTATTCATCGGCTCAACACATCGTGATT 309

seq\_name: gb\_est2:BE498178

seq\_documentation\_block:

LOCUS BE498178 432 bp mRNA linear EST 04-AUG-2000  
DEFINITION WHE0954\_E12\_J24ZS wheat pre-anthesis spike cDNA library Triticum aestivum cDNA clone WHE0954\_E12\_J24, mRNA sequence.

ACCESSION BE498178

VERSION BE498178.1 GI:9696795

KEYWORDS

EST.

SOURCE

bread wheat.

ORGANISM

Triticum aestivum

REFERENCE

1 (bases 1 to 432)

AUTHORS

Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L. and Tong,J.C.

TITLE

The structure and function of the expressed portion of the wheat genomes - Pre-anthesis spike cDNA library

JOURNAL

unpublished (2000)

COMMENT

Contact: Olin Anderson  
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center  
800 Buchanan Street, Albany, CA 94710, USA  
Tel: 5105595773  
Fax: 5105595818

FEATURES

Source

1.432

Location/Qualifiers

source

/organism="Triticum aestivum"

/cultivar="Chinese Spring"

/db\_xref="taxon:4565"

/clone="WHE0954\_E12\_J24"

/clone\_1lb="Wheat pre-anthesis spike cDNA library"

/tissue\_type="Spike before anthesis"

/dev\_stage="Adult plant"

/lab\_host="E. coli SOLR"

/note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site.1: EcoRI; Site.2: XhoI; Plants were grown in the greenhouse. Whole spike with awns trimmed, white, green and yellow anther were collected and total RNA, and poly(A) RNA were prepared, a cDNA library was made, and

the cDNA clones were in vivo excised to give pBluescript phagemids in the T3 Close Lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

BASE COUNT 118 a 103 c 138 g 73 t

ORIGIN

alignment\_scores:

Quality:	28.00	Length:	28
Ratio:	1.000	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	100.000

alignment\_block:

US-09-805-550-4 x BE498178 ..

Align seg 1/1 to: BE498178 from: 1 to: 432

20 AsnAspThrIleMetAlaValLysAsnIleGluGlnIleGlnGly 36  
|||||  
268 AATGACACCATATGCTGCTCAGAGAACATTCAGATTCAGAGAAA 317

36 SASPSerTyrProTrrpGlyGlnGlnLeuIle 47  
|||||  
318 GGATAGTATTCATCGGCTCAACACATCGTGATT 351

seq\_name: gb\_est2:BE517807

seq\_documentation\_block:

LOCUS BE517807 448 bp mRNA linear EST 08-AUG-2000  
DEFINITION WHE0803\_E10\_J19ZS wheat vernalized crown cDNA library Triticum aestivum cDNA clone WHE0803\_E10\_J19, mRNA sequence.

ACCESSION BE517807

VERSION BE517807.1 GI:9741837

KEYWORDS

EST.

SOURCE

bread wheat.

ORGANISM

Triticum aestivum

REFERENCE

1 (bases 1 to 448)

AUTHORS

Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L. and Tong,J.C.

TITLE

The structure and function of the expressed portion of the wheat genomes - Vernalized crown cDNA library

JOURNAL

unpublished (2000)

COMMENT

Contact: Olin Anderson  
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center  
800 Buchanan Street, Albany, CA 94710, USA  
Tel: 5105595773  
Fax: 5105595818

FEATURES

Source

1.448

Location/Qualifiers

source

/organism="Triticum aestivum"

/cultivar="Chinese Spring"

/db\_xref="taxon:4565"

/clone="WHE0803\_E10\_J19"

/clone\_1lb="Wheat vernalized crown cDNA library"

/tissue\_type="Crown tissue of seedling"

/dev\_stage="Five-week old seedling"

/lab\_host="E. coli SOLR"

/note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site.1: EcoRI; Site.2: XhoI; Seeds were germinated and grown at 4 C for 5 weeks. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made, and

the cDNA clones were in vivo excised to give pBluescript

phagemids in the T1 Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

BASE COUNT

120 a 108 c 146 g 74 t

# alignment\_scores:

Quality: 28.00 Length: 28  
Ratio: 1.000 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

# alignment\_block:

US-09-805-550-4 x BE517807 ..

Align seg 1/1 to: BE517807 from: 1 to: 448

20 AsnAspThrIleMetAlaValLysAsnIleGlnIleGlnGly 36  
|||||  
286 AATGACACCATTTATGCTGTCAAGAACATTTGAGAGATTCAAGGAA 335

36 sAspSerTyrProTrpGlyGlnGlnLeuLeu 47  
|||||  
336 GGATAGTTATCCGTGGGCTCAACAACACTGCTGATT 369

seq\_name: gb\_est2:BE585808

# seq\_documentation\_block:

LOCUS BE585808 725 bp mRNA linear EST 17-AUG-2000  
DEFINITION Est#2PT7\_E07\_e7\_051 KSU wheat Fusarium graminearum infected spike  
CDNA library Triticum aestivum CDNA clone Est#2PT7\_E07\_e7\_051, mRNA  
sequence.

ACCESSION BE585808  
VERSION BE585808.1 GI:9838840  
KEYWORDS EST.

# SOURCE

ORGANISM Triticum aestivum  
broad wheat.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae  
; Triticeae; Triticum.  
1 (bases 1 to 725)  
Fellers,J.P., Li,W.L., Hill-Ambroz,K., Matthews,A. and Gill,B.S.  
The structure and function of the expressed portion of the wheat  
genomes - Kansas State University. Fusarium graminearum infected  
spike CDNA library  
Unpublished (2000)  
Contact: John Fellers  
US Department of Agriculture, Agriculture Research Service, Plant  
Science and Entomology Unit  
Dept. of Plant Pathology, 4006 Throckmorton Hall, Kansas State  
University, Manhattan, KS 66506, USA  
Tel: 785-532-2367  
Fax: 785-532-6167  
Email: jofell@alfalfa.ksu.edu

# REFERENCE

AUTHORS Fellers,J.P., Li,W.L., Hill-Ambroz,K., Matthews,A. and Gill,B.S.  
TITLE The structure and function of the expressed portion of the wheat  
genomes - Kansas State University. Fusarium graminearum infected  
spike CDNA library  
COMMENT Unpublished (2000)  
JOURNAL Contact: John Fellers  
US Department of Agriculture, Agriculture Research Service, Plant  
Science and Entomology Unit  
Dept. of Plant Pathology, 4006 Throckmorton Hall, Kansas State  
University, Manhattan, KS 66506, USA  
Tel: 785-532-2367  
Fax: 785-532-6167  
Email: jofell@alfalfa.ksu.edu

# JOURNAL

COMMENT Unpublished (2000)  
JOURNAL Contact: John Fellers  
US Department of Agriculture, Agriculture Research Service, Plant  
Science and Entomology Unit  
Dept. of Plant Pathology, 4006 Throckmorton Hall, Kansas State  
University, Manhattan, KS 66506, USA  
Tel: 785-532-2367  
Fax: 785-532-6167  
Email: jofell@alfalfa.ksu.edu

# FEATURES

source

1. 725  
Location/Qualifiers

/organism="Triticum aestivum"

/cultivar="Suma13"

/db\_xref="taxon:4565"

/clone="Est#2PT7\_E07\_e7\_051"

/clone\_lib="KSU wheat Fusarium graminearum infected spike  
CDNA library"

/tissue\_type="Spoke"

/dev\_stage="Adult plant"

/lab\_host="E. coli JM109"

/note="Vector: pGEM-T easy; Site:1: SacII; Site:2: SpeI;  
Plants were grown in the greenhouse. Spikes were sprayed  
with Fusarium graminearum (at what stage). Total RNA, and  
poly(A) RNA were prepared from infected spikes. CDNA was

prepared using the SmartTM PCR cDNA synthesis kit from  
Clontech. CDNA was cloned into the pGEM-T easy vector  
from Promega."

BASE COUNT

197 a 196 c 203 g 128 t 1 others

# alignment\_scores:

Quality: 28.00 Length: 28  
Ratio: 1.000 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

# alignment\_block:

US-09-805-550-4 x BE585808 ..

Align seg 1/1 to: BE585808 from: 1 to: 725

20 AsnAspThrIleMetAlaValLysAsnIleGlnIleGlnGly 36  
|||||  
327 AATGACACCATTTATGCTGTCAAGAACATTTGAGAGATTCAAGGAA 376

36 sAspSerTyrProTrpGlyGlnGlnLeuLeu 47  
|||||  
377 GGATAGTTATCCGTGGGCTCAACAACACTGCTGATT 410

seq\_name: gb\_est2:BG629728

# seq\_documentation\_block:

LOCUS BG629728 418 bp mRNA linear EST 19-APR-2001  
DEFINITION cc-eflicEL29M16al Tomato flower library from a mixture of  
developmental stages Lycopersicon esculentum CDNA clone  
cc-eflicEL29M16al, mRNA sequence.

ACCESSION BG629728  
VERSION BG629728.1 GI:13681214  
KEYWORDS EST.

# SOURCE

ORGANISM Lycopersicon esculentum  
tomato.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asterales; eusteoids I; Solanales; Solanaceae; Solanum;  
Lycopersicon.  
1 (bases 1 to 418)  
van der Hoeven,R.S. and Tanksley,S.D.  
ESTs from a tomato flower library  
Unpublished (2001)  
Contact: Rutgers S. van der Hoeven  
Cornell University  
252 Emerson Hall, Ithaca, NY 14850, USA  
Tel: 607 255 7886  
Fax: 607 255 6883  
Email: rv19@cornell.edu

# REFERENCE

AUTHORS van der Hoeven,R.S. and Tanksley,S.D.  
TITLE ESTs from a tomato flower library  
JOURNAL Unpublished (2001)  
COMMENT Contact: Rutgers S. van der Hoeven  
Cornell University  
252 Emerson Hall, Ithaca, NY 14850, USA  
Tel: 607 255 7886  
Fax: 607 255 6883  
Email: rv19@cornell.edu

# JOURNAL

COMMENT Unpublished (2001)  
JOURNAL Contact: Rutgers S. van der Hoeven  
Cornell University  
252 Emerson Hall, Ithaca, NY 14850, USA  
Tel: 607 255 7886  
Fax: 607 255 6883  
Email: rv19@cornell.edu

# FEATURES

source

1. 418  
Location/Qualifiers

/organism="Lycopersicon esculentum"

/cultivar="E6203"

/db\_xref="taxon:4081"

/clone="cc-eflicEL29M16al"

/clone\_lib="Tomato flower library from a mixture of  
developmental stages"

/tissue\_type="developing flower buds and open flowers"

/dev\_stage="4-8 week old plants"

/lab\_host="XL0LR"

/note="Vector: pBK CMV; Site:1: EcoRI; Site:2: XhoI;  
Flowers and flower buds were collected from greenhouse  
grown plants and used for library construction (cLEL)."

BASE COUNT

126 a 101 c 58 g 133 t

# alignment\_scores:

Quality: 24.00 Length: 24  
Ratio: 1.000 Gaps: 0



Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-805-550-4 x BG629728/rev ..

Align seg 1/1 to reverse of: BG629728 from: 1 to: 418

```
342 ValIleGIuAlaPheLeuAlaCysAspArgAsnGIuGIuLeuAlaAlaAs 358
|||||
238 GTCATTGAGAGCTTTTGTGCTGTGTCGCAATGAGAACTGGCTGCCAA 189
|||||
358 nTyrLeuEnGIuHisAlaGIy 365
|||||
188 TTATCTGTTGGAGCATGCAGGA 167
```

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